Supplementary Information

Contents

Supplementary figure legends

Figure S1. Cana was harmless to mice renal function. (**A**) The levels of BUN in kidney. (B) Serum lipid from the indicated group were assayed.

Figure S2. Cana was innoxious to kidney in WT *Atg7*$^{\mathbf{cKO}}$ mice. Mice received intragastric administration of saline or Cana (20 mg/kg). (**A**) Representative microphages for H&E and Sirius Red staining of kidney sections.

Figure S3. The effect of FTO on autophagy. (A) HK2 cells were transfected with a tandem mRFP-GFP-LC3 construct for 24 h and then received the indicated treatments. Representative micrographs of the indicated cells were shown.

Figure S4. SQSTM1 mRNA was predicted as the target of FTO. (**A**) Online predictive tool (SRAMP, http://www.cuilab.cn/sramp) revealed the potential m6A methylation sites with high probability. (**B**) AUGGACU were the binding sites or motif of FTO. (**C**) The potential m6A methylation sites of SQSTM1 mRNA were identified with very high confidence.

Figure S5. Cana was harmless to WT or renal tubular SQSTM1 deletion mice. (**A**) Representative microphages for H&E and Sirius Red staining of kidney sections with indicated treatments.

Supplementary primer list

Table 1

Primer Sequence (5’-3’)		
h-FN	Forward	TGGCTGTCAGTCAAAGCAAG
	Reverse	CTCGGCTTCCTCCATAACAA
h-α-SMA	Forward	CAGCCAAGCACTGTCAGG
	Reverse	CCAGAGCCATTGTCACACAC
h-TGFβ	Forward	GTACCTGAACCCGTGTTGCT
	Reverse	GTATCGCCAGGAATTGTTGC
h-METTL3	Forward	TTGTCTCCAACCTTCCGTAGT
	Reverse	CCAGATCAGAGAGGTGGTGTAG
h-METTL14	Forward	CTGAGAGTGCGGATAGCATTG
	Reverse	GAGCAGATGTATCATAGGAAGCC
h-FTO	Forward	ACTTGGCTCCCTTATCTGACC
	Reverse	TGTGCAGTGTGAGAAAGGCTT
h-ALKBH5	Forward	CGGCGAAGGCTACACTTACG
	Reverse	CCACCAGCTTTTGGATCACCA
h-WTAP	Forward	CTTCCCAAGAAGGTTCGATTGA
	Reverse	TCAGACTCTCTTAGGCCAGTTAC
h- SREBP-1c	Forward	TGCATTTTCTGACACGCTTC
	Reverse	CCAAGCTGTACAGGCTCTCC
h- SREBP-2	Forward	CCGCCTGTTCCGATGTACAC

	Reverse	TGCACATTCAGCCAGGTTCA
h- FASN	Forward	GGAAGCTGCCAGAGTCGGAGAACT
	Reverse	TGAGGGTCCATCGTGTGTGCCT
h- PPARα	Forward	ATGGTGGACACGGAAAGCC
	Reverse	CGATGGATTGCGAAATCTCTTGG
h- ACOX-1	Forward	CCAAGCTTTCCTGCTCAGTGTT
	Reverse	CCCCCAGTCCCTTTTCTTCA
h-GAPDH	Forward	CTGACTTCAACAGCGACACC
	Reverse	TGCTGTAGCCAAATTCGTTGT
h-CPT-1α	Forward	TCGTCACCTCTTCTGCCTTT
	Reverse	ACACACCATAGCCGTCATCA
h-CD36	Forward	GGCTTAATGAGACTGGGACCA
	Reverse	TCACCACACCAACACTGAGT
h-FATP1	Forward	TGACGTGCTCTATGACTGCC
	Reverse	ACTTGATGCAGTCGTCCCAG
h-APOA4	Forward	GGTGACCTGCAGAAGAAGCT
	Reverse	CCAGCTCCTTCCCAATCTCC
h-MTTP	Forward	ATACCTGCAGCCTGACAACC
	Reverse	TTCTTCGCAGTCCTGAGGTG
h-STAT6	Forward	CACCGAGGGAATGGCGCACCGTTTG
	Reverse	AAACCAAACGGTGCGCCATTCCCTC
h-Arginase1	Forward	GGCTGGTCTGCTTGAGAAAC

	Reverse	TTCCCACAGACCTTGGATTC
m-β-actin	Forward	AAGGCCAACCGTGAAAAGAT
	Reverse	GTGGTACGACCAGAGGCATAC
m-FN	Forward	CATGAAGGGGGTCAGTCCTA
	Reverse	TAGGTTTGCAGGTCCATTCC
m-α-SMA	Forward	GTCCCAGACATCAGGGAGTAA
	Reverse	TCGGATACTTCAGCGTCAGGA
m-TGF-β1	Forward	GACTCTCCACCTGCAAGACC
	Reverse	GACTGGCGAGCCTTAGTTTG
m-METTL14	Forward	CTGAGAGTGCGGATAGCATTG
	Reverse	GAGCAGATGTATCATAGGAAGCC
m-FTO	Forward	TTCATGCTGGATGACCTCAATG
	Reverse	GCCAACTGACAGCGTTCTAAG
m-ALKBH5	Forward	CGCGGTCATCAACGACTACC
	Reverse	ATGGGCTTGAACTGGAACTTG
m-WTAP	Forward	GAACCTCTTCCTAAAAAGGTCCG
	Reverse	TTAACTCATCCCGTGCCATAAC
m- SREBP-1c	Forward	GGGCAAGTACACAGGAGGAC
	Reverse	AGATCTCTGCCAGTGTTGCC
m- SREBP-2	Forward	CAGGCGACCAGGAAGAAGAG
	Reverse	CGGAACTGCTGGAGAATGGT
m- FASN	Forward	GACCTCAGGCTGCAGTGAAT

	Reverse	CACCTTCTTGAGAGCCTGCA
m- PPARα	Forward	AGTGCCCTGAACATCGAGTG
	Reverse	TTGCAGCTCCGATCACACTT
m- ACOX-1	Forward	GGGGAACATCATCACAGGGG
	Reverse	ATCATAGCGGCCGAGAACAG
m-CPT-1α	Forward	TTGGACGAATCGGAACAGGG
	Reverse	CCATGCAGCAGAGATTTGGC
m-CD36	Forward	ATTGTACCTGGGAGTTGGCG
	Reverse	CAGCCAGGACTGCACCAATA
m-FATP1	Forward	CGCCGATGTGCTCTATGACT
	Reverse	ACACAGTCATCCCAGAAGCG
m-APOA4	Forward	GGAGCACCTGAAGCCCTATG
	Reverse	CATCATCGAGGTGTGCAGGT
m-MTTP	Forward	AATGCGGGTCAACAGAGAGG
	Reverse	CCCCGGACCAGATGAAGAAG
m-STAT6	Forward	GATGACTGTGGAAAGGGACCA
	Reverse	GGATGGACTGTGGAGGATACC
m-Arginase1	Forward	CGCCTTTCTCAAAAGGACAG
	Reverse	TTTTTCCAGCAGACCAGCTT

Figure S1

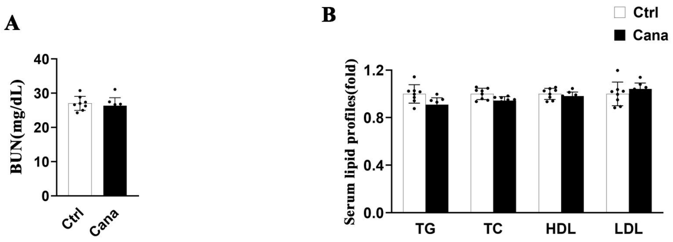
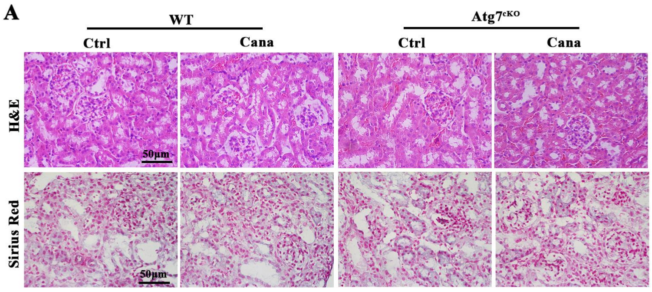

A
40
30
20
10
0
BUN(mg/dL)
Ctrl
Cana
B
☐ Ctrl
■ Cana
1.2
0.8
0.4
0.0
Serum lipid profiles(fold)
TG
TC
HDL
LDL

Figure S2



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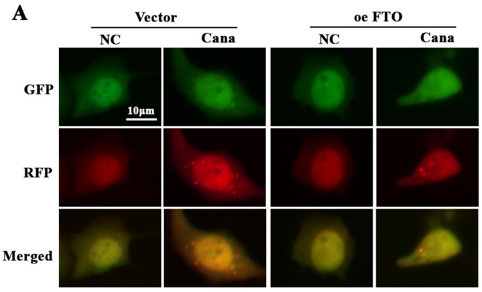

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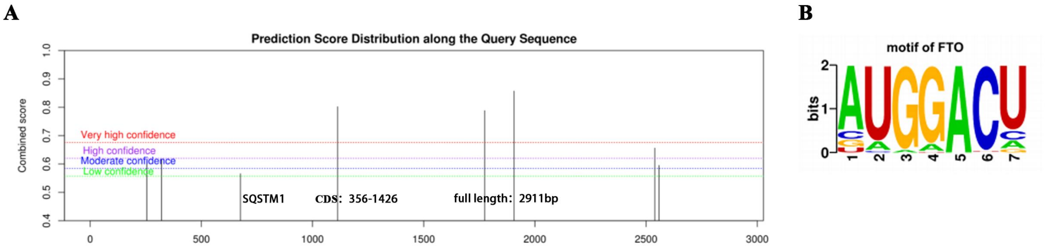
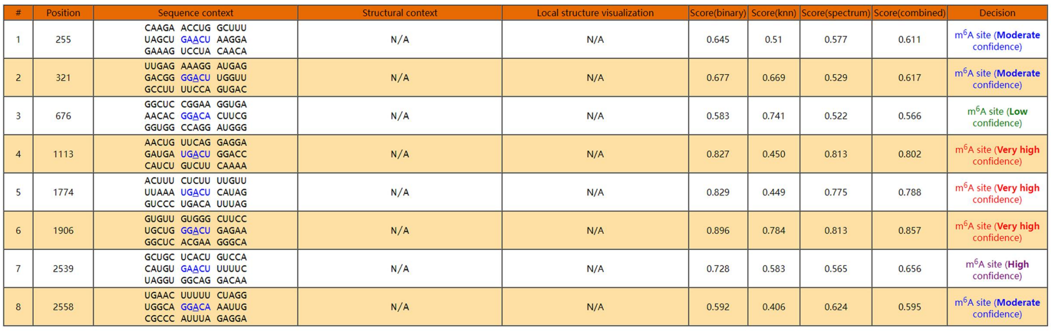


C



#	Position	Sequence context	Structural context	Local structure visualization	Score(binary)	Score(knn)	Score(spectrum)	Score(combined)	Decision
1	255	CAAGA ACCUG GCUUU UAGCU GAACU AAGGA GAAAG UCCUA CAACA	N/A	N/A	0.645	0.51	0.577	0.611	m^6A site (**Moderate** confidence)
2	321	UUGAG AAAGG AUGAG GACGG GGACU UGGUU GCCUU UUCCA GUGAC	N/A	N/A	0.677	0.669	0.529	0.617	m^6A site (**Moderate** confidence)
3	676	GGCUC CGGAA GGUGA AACAC GGACA CUUCG GGUGG CCAGG AUGGG	N/A	N/A	0.583	0.741	0.522	0.566	m^6A site (**Low** confidence)
4	1113	AACUG UUCAG GAGGA GAUGA UGACU GGACC CAUCU GUCUU CAAAA	N/A	N/A	0.827	0.450	0.813	0.802	m^6A site (**Very high** confidence)
5	1774	ACUUU CUCUU UUGUU UUAAA UGACU CAUAG GUCCC UGACA UUUAG	N/A	N/A	0.829	0.449	0.775	0.788	m^6A site (**Very high** confidence)
6	1906	GUGUU GUGGG CUUCC UGCUG GGACU GAGAA GGCUC ACGAA GGGCA	N/A	N/A	0.896	0.784	0.813	0.857	m^6A site (**Very high** confidence)
7	2539	GCUGC UCACU GUCCA CAUGU GAACU UUUUC UAGGU GGCAG GACAA	N/A	N/A	0.728	0.583	0.565	0.656	m^6A site (**High** confidence)
8	2558	UGAAC UUUUU CUAGG UGGCA GGACA AAUUG CGCCC AUUUA GAGGA	N/A	N/A	0.592	0.406	0.624	0.595	m^6A site (**Moderate** confidence)

Figure S5